



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Björck, Lars
Sjöbring, Ulf

(ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Seed IP Law Group
(B) STREET: 701 Fifth Avenue Suite 6300
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/325,278
(B) FILING DATE: 26-OCT-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Potter, Jane E. R.
(B) REGISTRATION NUMBER: 33,332
(C) REFERENCE/DOCKET NUMBER: 100084.402

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
 1 5 10 15
 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
 20 25 30
 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
 35 40 45
 Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
 50 55 60
 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 65 70 75 80
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 85 90 95
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 100 105 110
 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 115 120 125
 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 130 135 140
 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
 145 150 155 160
 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
 165 170 175
 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
 180 185 190
 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
 195 200 205
 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 210 215 220
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 225 230 235 240
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 245 250 255
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 260 265 270
 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 275 280 285

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
 290 295 300

Glu
 305

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA 60
 ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAAGTGCAGA ATTCAAAGGA 120
 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT 180
 GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA 240
 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT 300
 GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA 360
 GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA 420
 GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA 480
 AAAGAAGAAG TTACTATTAA AGCAAACCTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA 540
 GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGAATTATTA 600
 GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT 660
 AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA 720
 AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA 780
 GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA 840
 GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC 900
 GAAAAACCAG AAGAATAATA A 921

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
 1 5 10 15
 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
 20 25 30
 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
 35 40 45
 Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
 50 55 60
 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 65 70 75 80
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 85 90 95
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 100 105 110
 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 115 120 125
 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 130 135 140
 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
 145 150 155 160
 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
 165 170 175
 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
 180 185 190
 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
 195 200 205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 210 215 220
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 225 230 235 240
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 245 250 255
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 260 265 270
 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 275 280 285
 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
 290 295 300
 Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
 305 310 315 320
 Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
 325 330 335
 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
 340 345 350
 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
 355 360 365
 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
 370 375 380
 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
 385 390 395 400
 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
 405 410 415
 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
 420 425 430
 Glu Met

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli* L392/pHDLG, DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA 60
 ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AACTGCAGA ATTCAAAGGA 120
 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT 180
 GGAGAATATA CTGTAGATGT TGCAGATAAA GGTATACTT TAAATATTAA ATTTGCTGGA 240
 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAA CTTAATCTAT 300
 GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA 360
 GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA 420
 GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA 480
 AAAGAAGAAG TTACTATTAA AGCAAACCTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA 540
 GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTIONATTA 600
 GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT 660
 AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAG AAGAAGTTAC TATTAAAGCA 720
 AACTTAATCT ATGCAGATGG AAAAATCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA 780
 GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA 840
 GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC 900
 GAAAAACCAG AAGAACCCAT GGACACTTAC AAATTAATCC TTAATGGTAA AACATTGAAA 960
 GGCGAAACAA CTACTIONAAGC TGTTGATGCT GCTACTGCAG AAAAAGTCTT CAAACAATAC 1020
 GCTAACGACA ACGGTGTTGA CGGTGAATGG ACTTACGACG ATGCGACTAA GACCTTTACA 1080
 GTTACTGAAA AACCAGAAGT GATCGATGCG TCTGAATTAA CACCAGCCGT GACAACTTAC 1140
 AAATTGTTA TTAATGGTAA AACATTGAAA GGCGAAACAA CTACTIONAAGC AGTAGACGCA 1200
 GAAACTGCAG AAAAAGCCTT CAAACAATAC GCTAACGACA ACGGTGTTGA TGGTGTGTTG 1260
 ACTTATGATG ATGCGACTAA GACCTTTACG GTACTIONAAA TGTAAATA 1308

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC	48
Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn	
1 5 10 15	
AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA	96
Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu	
20 25 30	
AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG	144
Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys	
35 40 45	
AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT	192
Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg	
50 55 60	
AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA	240
Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu	
65 70 75 80	
GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA	288
Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu	
85 90 95	
GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG	336
Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg	
100 105 110	
GAC TAC CAT AGA GCT ACC GCT TTA GAA AAA GAG TTA GAA GAG AAA AAG	384
Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Glu Lys Lys	
115 120 125	
AAA GCT CTT GAA TTA GCG ATA GAC CAA GCG AGT CAG GAC TAT AAT AGA	432
Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg	
130 135 140	
GCT AAC GTC TTA GAA AAA GAG TTA GAA ACG ATT ACT AGA GAA CAA GAG	480
Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu	
145 150 155 160	
ATT AAT CGT AAT CTT TTA GGC AAT GCA AAA CTT GAA CTT GAT CAA CTT	528
Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu	

165								170				175				
TCA Ser	TCT Ser	GAA Glu	AAA Lys 180	GAG Glu	CAG Gln	CTA Leu	ACG Thr	ATC Ile 185	GAA Glu	AAA Lys	GCA Ala	AAA Lys	CTT Leu 190	GAG Glu	GAA Glu	576
GAA Glu	AAA Lys	CAA Gln 195	ATC Ile	TCA Ser	GAC Asp	GCA Ala	AGT Ser 200	CGT Arg	CAA Gln	AGC Ser	CTT Leu	CGT Arg 205	CGT Arg	GAC Asp	TTG Leu	624
GAC Asp	GCA Ala 210	TCA Ser	CGT Arg	GAA Glu	GCT Ala	AAG Lys 215	AAA Lys	CAG Gln	GTT Val	GAA Glu	AAA Lys 220	GAT Asp	TTA Leu	GCA Ala	AAC Asn	672
TTG Leu 225	ACT Thr	GCT Ala	GAA Glu	CTT Leu	GAT Asp 230	AAG Lys	GTT Val	AAA Lys	GAA Glu	GAC Asp 235	AAA Lys	CAA Gln	ATC Ile	TCA Ser	GAC Asp 240	720
GCA Ala	AGC Ser	CGT Arg	CAA Gln 245	CGG Arg	CTT Leu	CGC Arg	CGT Arg	GAC Asp	TTG Leu 250	GAC Asp	GCA Ala	TCA Ser	CGT Arg	GAA Glu 255	GCT Ala	768
AAG Lys	AAA Lys	CAG Gln 260	GTT Val	GAA Glu	AAA Lys	GAT Asp	TTA Leu	GCA Ala 265	AAC Asn	TTG Leu	ACT Thr	GCT Ala 270	GAA Glu	CTT Leu	GAT Asp	816
AAG Lys	GTT Val 275	AAA Lys	GAA Glu	GAA Glu	AAA Lys	CAA Gln	ATC Ile 280	TCA Ser	GAC Asp	GCA Ala	AGC Ser	CGT Arg 285	CAA Gln	CGG Arg	CTT Leu	864
CGC Arg 290	CGT Arg	GAC Asp	TTG Leu	GAC Asp	GCA Ala	TCA Ser 295	CGT Arg	GAA Glu	GCT Ala	AAG Lys	AAA Lys 300	CAA Gln	GTT Val	GAA Glu	AAA Lys	912
GCT Ala 305	TTA Leu	GAA Glu	GAA Glu	GCA Ala	AAC Asn 310	AGC Ser	AAA Lys	TTA Leu	GCT Ala 315	GCT Ala	CTT Leu	GAA Glu	AAA Lys	CTT Leu	AAC Asn 320	960
AAA Lys	GAG Glu	CTT Leu	GAA Glu 325	GAA Glu	AGC Ser	AAG Lys	AAA Lys	TTA Leu 330	ACA Thr	GAA Glu	AAA Lys	GAA Glu	AAA Lys 335	GCT Ala	GAA Glu 340	1008
CTA Leu	CAA Gln	GCA Ala	AAA Lys 340	CTT Leu	GAA Glu	GCA Ala	GAA Glu	GCA Ala 345	AAA Lys	GCA Ala	CTC Leu	AAA Lys 350	GAA Glu	CAA Gln	TTA Leu	1056
GCG Ala	AAA Lys	CAA Gln 355	GCT Ala	GAA Glu	GAA Glu	CTC Leu	GCA Ala 360	AAA Lys	CTA Leu	AGA Arg	GCT Ala 365	GGA Gly	AAA Lys	GCA Ala	TCA Ser	1104
GAC Asp	TCA Ser 370	CAA Gln	ACC Thr	CCT Pro	GAT Asp	ACA Thr 375	AAA Lys	CCA Pro	GGA Gly	AAC Asn	AAA Lys 380	GCT Val	CTT Leu	CCA Pro	GGT Gly	1152
AAA Lys 385	GGT Gly	CAA Gln	GCA Ala	CCA Pro	CAA Gln 390	GCA Ala	GGT Gly	ACA Thr	AAA Lys 395	CCT Pro	AAC Asn	CAA Gln	AAC Asn	AAA Lys	GCA Ala 400	1200

CCA ATG AAG GAA ACT AAG AGA CAG TTA CCA TCA ACA GGT GAA ACA GCT	1248
Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala	
405 410 415	
AAC CCA TTC TTC ACA GCG GCA CGC GTT ACT GTT ATG GCA ACA GCT GGA	1296
Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly	
420 425 430	
GTA GCA GCA GTT GTA AAA CGC AAA GAA GAA AAC TAA	1332
Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn	
435 440	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn
1 5 10 15

Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu
20 25 30

Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys
35 40 45

Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg
50 55 60

Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu
65 70 75 80

Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu
85 90 95

Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg
100 105 110

Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Glu Lys Lys
115 120 125

Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg
130 135 140

Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu
145 150 155 160

Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu
165 170 175

Ser Ser Glu Lys Glu Gln Leu Thr Ile Glu Lys Ala Lys Leu Glu Glu
 180 185 190
 Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Ser Leu Arg Arg Asp Leu
 195 200 205
 Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys Asp Leu Ala Asn
 210 215 220
 Leu Thr Ala Glu Leu Asp Lys Val Lys Glu Asp Lys Gln Ile Ser Asp
 225 230 235 240
 Ala Ser Arg Gln Arg Leu Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala
 245 250 255
 Lys Lys Gln Val Glu Lys Asp Leu Ala Asn Leu Thr Ala Glu Leu Asp
 260 265 270
 Lys Val Lys Glu Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Arg Leu
 275 280 285
 Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys
 290 295 300
 Ala Leu Glu Glu Ala Asn Ser Lys Leu Ala Ala Leu Glu Lys Leu Asn
 305 310 315 320
 Lys Glu Leu Glu Glu Ser Lys Lys Leu Thr Glu Lys Glu Lys Ala Glu
 325 330 335
 Leu Gln Ala Lys Leu Glu Ala Glu Ala Lys Ala Leu Lys Glu Gln Leu
 340 345 350
 Ala Lys Gln Ala Glu Glu Leu Ala Lys Leu Arg Ala Gly Lys Ala Ser
 355 360 365
 Asp Ser Gln Thr Pro Asp Thr Lys Pro Gly Asn Lys Ala Val Pro Gly
 370 375 380
 Lys Gly Gln Ala Pro Gln Ala Gly Thr Lys Pro Asn Gln Asn Lys Ala
 385 390 395 400
 Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala
 405 410 415
 Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly
 420 425 430
 Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn
 435 440

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTCAGGCGG CGCCGGTAGA AAATAAAGAA GAAACACCAG AAAC

44

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Glu Asn Lys Glu Glu Thr Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCAGCAGG ATTCTTATTA TTCTTCTGGT TTTTCGTCAA CTTTCTT

47

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGCAGCAGC CATGGGTTCT TCTGGTTTTT CGTCAACTTT CTTA

44

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCATGGAC ACTTACAAAT TAATCCTTAA TGGT

34

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAGGTCGACT TATTACATTT CAGTTACCGT AAAGGTCTTA GT

42

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCTTAAGG AGGTTAATCG ATGAAAAAAAA CTGCTATCGC TATCGCTGTT GCTCTGGCTG 60
GTTTCGCTAC TGTGCTCAG GCGGCGCCGA GATCTAAACA GGAATTCGAG CTCGGTACCC 120
GGGGATCCTC TAGAGCTGAC CTGCAGGCAT GC 152

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Val Glu Asn
1
